

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-9. (Canceled)

10. (Previously presented) A method for biasing a DNA amplification reaction such that a first nucleic acid molecule having a first nucleotide present at a polymorphic site is amplified to a greater extent than a second nucleic acid molecule having a second, different nucleotide present at the polymorphic site, comprising

(a) contacting a sample of DNA comprising at least the first nucleic acid molecule with two amplification primers that hybridize to both the first nucleic acid molecule and the second nucleic acid molecule at locations which flank the polymorphic site such that neither the first primer nor the second primer hybridizes to the polymorphic site, one of the two primers including a 5' portion which, when incorporated into an amplification product, will upon further amplification yield products that form a stable stem-loop structure, the stem of which is perfectly matched and includes the polymorphic site only when the second nucleotide is present at the polymorphic site, but not when the first nucleotide is present at the polymorphic site; and

(b) carrying out an amplification reaction, whereby the first nucleic acid molecule is amplified to a greater extent than the second nucleic acid molecule.

11. (Previously presented) The method of claim 10, wherein the DNA is single-stranded DNA.

12. (Previously presented) The method of claim 10, wherein the DNA is double-stranded DNA.

13. (Previously presented) The method of claim 10 further comprising separately carrying out steps (a) and (b) for each of a plurality of polymorphic sites.

14. (Previously presented) The method of claim 10 wherein the sample of DNA comprises mammalian DNA.

15. (Previously presented) The method of claim 14 wherein the sample of DNA comprises human DNA.

16. (Previously presented) A method for haplotyping a first nucleic acid molecule having a first nucleotide present at a polymorphic site present in a sample of DNA comprising at least the first nucleic acid molecule and a second nucleic acid molecule having a second, different nucleotide present at the polymorphic site, comprising:

(a) contacting a sample of DNA comprising at least the first nucleic acid molecule with two amplification primers that hybridize to both the first nucleic acid molecule and the second nucleic acid molecule at locations which flank the polymorphic site such that neither the first primer nor the second primer hybridizes to the polymorphic site, one of the two primers including a 5' portion which, when incorporated into an amplification product, will upon further amplification yield products that form a stable stem-loop structure, the stem of which is perfectly matched and includes the polymorphic site only when the second nucleotide is present at the polymorphic site, but not when the first nucleotide is present at the polymorphic site;

(b) carrying out an amplification reaction, whereby the first nucleic acid molecule is amplified to a greater extent than the second nucleic acid molecule to create an amplified DNA sample; and

(c) determining the nucleotide sequence of at least a portion of the DNA present in the amplified DNA sample.